

RAW SEQUENCE LISTING

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Application Serial Number: 10/527,438 A
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DATE: 07/10/2006

PATENT APPLICATION: US/10/527,438A

TIME: 09:53:36

Input Set : A:\Sequence Listing 06-03.txt

Output Set: N:\CRF4\07102006\J527438A.raw

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3 <110> APPLICANT: KOREA RESEARCH INSTITUTE OF BIOSCIENCE AND BIOTECHNOLOGY
4     CHOI, Eui-Sung
5     SOHN, Jung-Hoon
6     KIM, So-Young
8 <120> TITLE OF INVENTION: METHOD FOR SCREENING OF A LIPASE HAVING IMPROVED ENZYMATIC
9     ACTIVITY USING YEAST SURFACE DISPLAY VECTOR AND THE LIPASE
11 <130> FILE REFERENCE: 26666U
13 <140> CURRENT APPLICATION NUMBER: 10/527,438A
14 <141> CURRENT FILING DATE: 2005-03-11
16 <150> PRIOR APPLICATION NUMBER: KR 2002-55575
17 <151> PRIOR FILING DATE: 2002-09-13
19 <160> NUMBER OF SEQ ID NOS: 18
21 <170> SOFTWARE: PatentIn version 3.2
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 27
25 <212> TYPE: DNA
26 <213> ORGANISM: Artificial Sequence
28 <220> FEATURE:
29 <223> OTHER INFORMATION: CALB primer 1
31 <400> SEQUENCE: 1
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35 <210> SEQ ID NO: 2
36 <211> LENGTH: 23
37 <212> TYPE: DNA
38 <213> ORGANISM: Artificial Sequence
40 <220> FEATURE:
41 <223> OTHER INFORMATION: CALB primer 2
43 <400> SEQUENCE: 2
44 gcggatcctc agggggtgac gat 23
47 <210> SEQ ID NO: 3
48 <211> LENGTH: 27
49 <212> TYPE: DNA
50 <213> ORGANISM: Artificial Sequence
52 <220> FEATURE:
53 <223> OTHER INFORMATION: CALB primer 3
55 <400> SEQUENCE: 3
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59 <210> SEQ ID NO: 4
60 <211> LENGTH: 19
61 <212> TYPE: DNA
62 <213> ORGANISM: Artificial Sequence
64 <220> FEATURE:
65 <223> OTHER INFORMATION: GPD-err primer

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72 <211> LENGTH: 19
73 <212> TYPE: DNA
74 <213> ORGANISM: Artificial Sequence
76 <220> FEATURE:
77 <223> OTHER INFORMATION: T-O primer
79 <400> SEQUENCE: 5
80 tgcagttgaa cacaaccac                               19
83 <210> SEQ ID NO: 6
84 <211> LENGTH: 1023
85 <212> TYPE: DNA
86 <213> ORGANISM: Candida antarctica
89 <220> FEATURE:
90 <221> NAME/KEY: sig_peptide
91 <222> LOCATION: (1)..(51)
92 <223> OTHER INFORMATION: secretion signal
94 <400> SEQUENCE: 6
95 atgaatatat ttacatatt ttgtttttg ctgtcattcg ttcaaggtac cgccactccc      60
97 ttggtgaagc gtctgccttc cggttcggac cctgcctttt cgcagcccaa gtcggtgctc    120
99 gatgcggggtc tgacctgcca ggggtgcttcg ccactcctcg tctccaaacc catccttctc    180
101 gtccccggaa ccggcaccac aggtccacag tcgttcgact cgaactggat cccctctctc    240
103 gcgcagctgg gttacacacc ctgctggatc tcacccccgc cgttcatgct caacgacacc    300
105 caggtcaaca cggagtacat ggtcaacgcc atcaccacgc tctacgctgg ttcgggcaac    360
107 aacaagcttc ccgtgctcac ctgggtcccag ggtggtctgg ttgcacagtg gggctctgacc    420
109 ttcttcccca gtatcaggtc caaggtcgat cgacttatgg cctttgcgcc cgactacaag    480
111 ggcaccgttc tcgccggccc tctcgatgca ctgcgggta gtgcaccctc cgtatggcag    540
113 caaaccaccg gttcggcact cactaccgca ctccgaaacg caggtggtct gaccagatc    600
115 gtgccacca ccaacctcta ctcgcgacc gacgagatcg ttcagcctca ggtgtccaac    660
117 tcgccactcg actcatccta cctcttcaac gggaagaacg tccaggcaca ggctgtgtgt    720
119 gggccgctgt tcgtcatcga ccatgcaggc tcgtcacct cgcagttctc ctacgtcgtc    780
121 ggtcgatccg ccctgcgctc caccacgggc caggctcgta gtgcagacta tggcattacc    840
123 gactgcaacc ctcttcccgc caatgatctg actcccgagc aaaaggtcgc cgcggctgcg    900
125 ctcccggcgc cggcggtgc agccatcgty gcgggtccaa agcagaactg cgagcccgcac    960
127 ctcatgccct acgcccgcct ctttgacagta ggcaaaagga cctgctccgg catcgtcacc   1020
129 ccc                                                    1023
132 <210> SEQ ID NO: 7
133 <211> LENGTH: 1023
134 <212> TYPE: DNA
135 <213> ORGANISM: Candida antarctica
138 <220> FEATURE:
139 <221> NAME/KEY: sig_peptide
140 <222> LOCATION: (1)..(51)
141 <223> OTHER INFORMATION: secretion signal
143 <400> SEQUENCE: 7
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146 ttggtgaagc gtctgccttc cggttcggac cctgcctttt cgcagcccaa gtcggtgctc    120
148 gatgcggggtc tgacctgcca aggtgcttcg ccactcctcg tctccaaacc catccttctc    180

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150 gtccccggaa ccggcaccac aggtccacag tcgttcgact cgaactggat cccctctct 240
152 gcgcagctgg gttacacacc ctgctggatc tcacccccgc cgttcattgt caacgacacc 300
154 cagggtcaaca cggagtacat ggtcaacgcc atcaccacgc tctacgctgg ttcgggcaac 360
156 aacaagcttc ccgtgtcac ctgggtcccag ggtggtctgg ttgcacagtg ggtctgacc 420
158 ttcttcccca gtatcaggtc caaggtcgat cgacttatgg cctttgcgcc cgactacaag 480
160 ggcaccgtcc tcgccggccc tctcgatgca ctccgaaacg caggtggtct gacctagatc 540
162 caaaccaccg gttcggcact cactaccgca ctccgaaacg caggtggtct gacctagatc 600
164 gtgcccacca ccaacctcta ctccggcgacc gacgagatcg ttcagcctca ggtgtccaac 660
166 tcgccactcg actcatccta ccttttcaac ggaaagaacg tccaggcaca ggtgtgtgt 720
168 gggccgcagt tcgtcatcga ccatgcaggc tcgtcacct cgcagttctc ctacgtcgtc 780
170 ggtcgatccg cctgcgctc caccacgggc caggctcgta gtgcggacta tggcattacg 840
172 gactgcaacc ctcttccgc caatgatctg actcccgagc aaaaggctgc cgcggctgcg 900
174 ctcccggcgc cggcggtgc agccatcgtg gcgggtccaa agcagaactg cgagcccgcg 960
176 ctcatgccct acgcccgcct ctttgcagta ggcaaaagga cctgctccgg catcgtcacc 1020
178 ccc 1023

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181 <210> SEQ ID NO: 8

182 <211> LENGTH: 1023

183 <212> TYPE: DNA

184 <213> ORGANISM: Candida antarctica

187 <220> FEATURE:

188 <221> NAME/KEY: sig_peptide

189 <222> LOCATION: (1)..(51)

190 <223> OTHER INFORMATION: secretion signal

192 <400> SEQUENCE: 8

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193 atgaatatat ttacatatt ttgttttttg ctgtcattcg ttcaaggtag cgcactcct 60
195 ttggtgaagc gtctgccttc cggttcggac cctgcctttt cgcagcccaa gtcggtgctc 120
197 gatgcgggtc tgacctgcca ggggtgcttc ccactcctcg tctccaaacc catccttctc 180
199 gtccccggaa ccggcaccac aggtccacag tcgttcgact cgaactggat cccctctct 240
201 gcgcagctgg gttacacacc ctgctggatc tcacccccgc cgttcattgt caacgacacc 300
203 cagggtcaaca cggagtacat ggtcaacgcc atcaccacgc tctacgctgg ttcgggcaac 360
205 aacaagcttc ccgtgtcac ctgggtcccag ggtggtctgg ttgcacagtg ggtctgacc 420
207 ttcttcccca gtatcaggtc caaggtcgat cgacttatgg cctttgcgcc cgactacaag 480
209 ggcaccgtcc tcgccggccc tctcgatgca ctccgaaacg caggtggtct gacctagatc 540
211 caaaccaccg gttcggcact cactaccgca ctccgaaacg caggtggtct gacctagatc 600
213 gtgcccacca ccaacctcta ctccggcgacc gacgagatcg ttcagcctca ggtgtccaac 660
215 tcgccactcg actcatccta cctcttcaac ggaaagaacg tccaggcaca ggtgtgtgt 720
217 gggccgcagt tcgtcatcga ccatgcaggc tcgtcacct cgcagttctc ctacgtcgtc 780
219 ggtcgatccg cctgcgctc caccacgggc caggctcgta gtgcagacta tggcattacg 840
221 gactgcaacc ctcttccgc caatgatctg actcccgagc aaaaggctgc cgcggctgcg 900
223 ctcttggcgc cggcggtgc agccatcgtg gcgggtccaa agcagaactg cgagcccgcg 960
225 ctcatgccct acgcccgcct ctttgcagta ggcaaaagga cctgctccgg catcgtcacc 1020
227 ccc 1023

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230 <210> SEQ ID NO: 9

231 <211> LENGTH: 341

232 <212> TYPE: PRT

233 <213> ORGANISM: Candida antarctica

236 <220> FEATURE:

237 <221> NAME/KEY: SIGNAL

238 <222> LOCATION: (1)..(17)

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239 <223> OTHER INFORMATION: secretion signal

241 <400> SEQUENCE: 9

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243 Met Asn Ile Phe Tyr Ile Phe Leu Phe Leu Leu Ser Phe Val Gln Gly
244 1          5          10          15
247 Thr Ala Thr Pro Leu Val Lys Arg Leu Pro Ser Gly Ser Asp Pro Ala
248          20          25          30
251 Phe Ser Gln Pro Lys Ser Val Leu Asp Ala Gly Leu Thr Cys Gln Gly
252          35          40          45
255 Ala Ser Pro Ser Ser Val Ser Lys Pro Ile Leu Leu Val Pro Gly Thr
256          50          55          60
259 Gly Thr Thr Gly Pro Gln Ser Phe Asp Ser Asn Trp Ile Pro Leu Ser
260 65          70          75          80
263 Ala Gln Leu Gly Tyr Thr Pro Cys Trp Ile Ser Pro Pro Pro Phe Met
264          85          90          95
267 Leu Asn Asp Thr Gln Val Asn Thr Glu Tyr Met Val Asn Ala Ile Thr
268          100         105         110
271 Thr Leu Tyr Ala Gly Ser Gly Asn Asn Lys Leu Pro Val Leu Thr Trp
272          115         120         125
275 Ser Gln Gly Gly Leu Val Ala Gln Trp Gly Leu Thr Phe Phe Pro Ser
276          130         135         140
279 Ile Arg Ser Lys Val Asp Arg Leu Met Ala Phe Ala Pro Asp Tyr Lys
280 145         150         155         160
283 Gly Thr Val Leu Ala Gly Pro Leu Asp Ala Leu Ala Val Ser Ala Pro
284          165         170         175
287 Ser Val Trp Gln Gln Thr Thr Gly Ser Ala Leu Thr Thr Ala Leu Arg
288          180         185         190
291 Asn Ala Gly Gly Leu Thr Gln Ile Val Pro Thr Thr Asn Leu Tyr Ser
292          195         200         205
295 Ala Thr Asp Glu Ile Val Gln Pro Gln Val Ser Asn Ser Pro Leu Asp
296          210         215         220
299 Ser Ser Tyr Leu Phe Asn Gly Lys Asn Val Gln Ala Gln Ala Val Cys
300 225         230         235         240
303 Gly Pro Leu Phe Val Ile Asp His Ala Gly Ser Leu Thr Ser Gln Phe
304          245         250         255
307 Ser Tyr Val Val Gly Arg Ser Ala Leu Arg Ser Thr Thr Gly Gln Ala
308          260         265         270
311 Arg Ser Ala Asp Tyr Gly Ile Thr Asp Cys Asn Pro Leu Pro Ala Asn
312          275         280         285
315 Asp Leu Thr Pro Glu Gln Lys Val Ala Ala Ala Ala Leu Pro Ala Pro
316          290         295         300
319 Ala Ala Ala Ala Ile Val Ala Gly Pro Lys Gln Asn Cys Glu Pro Asp
320 305         310         315         320
323 Leu Met Pro Tyr Ala Arg Pro Phe Ala Val Gly Lys Arg Thr Cys Ser
324          325         330         335
327 Gly Ile Val Thr Pro
328          340
331 <210> SEQ ID NO: 10
332 <211> LENGTH: 341
333 <212> TYPE: PRT

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334 <213> ORGANISM: Candida antarctica

337 <220> FEATURE:

338 <221> NAME/KEY: SIGNAL

339 <222> LOCATION: (1)..(17)

340 <223> OTHER INFORMATION: secretion signal

342 <400> SEQUENCE: 10

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344 Met Asn Ile Phe Tyr Ile Phe Leu Phe Leu Leu Ser Phe Val Gln Gly
345 1          5          10          15
348 Thr Ala Thr Pro Leu Val Lys Arg Leu Pro Ser Gly Ser Asp Pro Ala
349          20          25          30
352 Phe Ser Gln Pro Lys Ser Val Leu Asp Ala Gly Leu Thr Cys Gln Gly
353          35          40          45
356 Ala Ser Pro Ser Ser Val Ser Lys Pro Ile Leu Leu Val Pro Gly Thr
357          50          55          60
360 Gly Thr Thr Gly Pro Gln Ser Phe Asp Ser Asn Trp Ile Pro Leu Ser
361 65          70          75          80
364 Ala Gln Leu Gly Tyr Thr Pro Cys Trp Ile Ser Pro Pro Pro Phe Met
365          85          90          95
368 Leu Asn Asp Thr Gln Val Asn Thr Glu Tyr Met Val Asn Ala Ile Thr
369          100         105         110
372 Thr Leu Tyr Ala Gly Ser Gly Asn Asn Lys Leu Pro Val Leu Thr Trp
373          115         120         125
376 Ser Gln Gly Gly Leu Val Ala Gln Trp Gly Leu Thr Phe Phe Pro Ser
377          130         135         140
380 Ile Arg Ser Lys Val Asp Arg Leu Met Ala Phe Ala Pro Asp Tyr Lys
381 145         150         155         160
384 Gly Thr Val Leu Ala Gly Pro Leu Asp Ala Leu Ala Val Ser Ala Pro
385          165         170         175
388 Ser Val Trp Gln Gln Thr Thr Gly Ser Ala Leu Thr Thr Ala Leu Arg
389          180         185         190
392 Asn Ala Gly Gly Leu Thr Gln Ile Val Pro Thr Thr Asn Leu Tyr Ser
393          195         200         205
396 Ala Thr Asp Glu Ile Val Gln Pro Gln Val Ser Asn Ser Pro Leu Asp
397          210         215         220
400 Ser Ser Tyr Leu Phe Asn Gly Lys Asn Val Gln Ala Gln Ala Val Cys
401 225         230         235         240
404 Gly Pro Gln Phe Val Ile Asp His Ala Gly Ser Leu Thr Ser Gln Phe
405          245         250         255
408 Ser Tyr Val Val Gly Arg Ser Ala Leu Arg Ser Thr Thr Gly Gln Ala
409          260         265         270
412 Arg Ser Ala Asp Tyr Gly Ile Thr Asp Cys Asn Pro Leu Pro Ala Asn
413          275         280         285
416 Asp Leu Thr Pro Glu Gln Lys Val Ala Ala Ala Ala Leu Pro Ala Pro
417          290         295         300
420 Ala Ala Ala Ala Ile Val Ala Gly Pro Lys Gln Asn Cys Glu Pro Asp
421 305         310         315         320
424 Leu Met Pro Tyr Ala Arg Pro Phe Ala Val Gly Lys Arg Thr Cys Ser
425          325         330         335
428 Gly Ile Val Thr Pro

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VERIFICATION SUMMARY

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